Please replace the paragraph at page 11, line 22 to page 12, line 10, as follows:

Figs. 2A and 2B depict the BAC/STS content physical map of the HBM region in 11q13.3. STS markers derived from genes, ESTs, microsatellites, random sequences, and BAC endsequences are denoted above the long horizontal line. For markers that are present in GDB the same nomenclature has been used. Locus names (D11S####) are listed in parentheses after the primary name if available. STSs derived from BAC endsequences are listed with the BAC name first followed by L or R for the left and right end of the clone, respectively. The two large arrows indicate the genetic markers that define the HBM critical region. The horizontal lines below the STSs indicate BAC clones identified by PCR-based screening of a nine-fold coverage BAC library. Open circles indicate that the marker did not amplify the corresponding BAC library address during library screening. Clone names use the following convention: B for BAC, the plate, row and column address, followed by -H indicating the HBM project (i.e., B36F16-H).

Please replace the paragraph at page 13, lines 8-12, as follows:

Figs. 6A-6J show the nucleotide and amino acid sequences (SEQ ID NOS: 1 and 3) of the wild-type gene, Zmax1. The location for the base pair substitution at nucleotide 582, a guanine to thymine, is underlined. This allelic variant is the *HBM* gene. The *HBM* gene encodes for a protein with an amino acid substitution of glycine to valine at position 171. The 5' untranslated region (UTR) boundaries bases 1 to 70, and the 3' UTR boundaries bases 4916-5120.

Please replace the paragraph at page 13, lines 17-18, as follows:

Figs. 10A and 10B show the cellular localization of mouse Zmax1 by *in situ* hybridization at 100X magnification using sense and antisense probes.

Please replace the paragraph at page 13, lines 19-20, as follows:

D5

Figs. 11A and 11B show the cellular localization of mouse Zmax1 by *in situ* hybridization at 400X magnification using sense and antisense probes.

Please replace the paragraph at page 13, lines 21-22, as follows:

D6

Figs. 12A and 12B show the cellular localization of mouse Zmax1 by *in situ* hybridization of osteoblasts in the endosteum at 400X magnification using sense and antisense probes.

Please replace the paragraph at page 75, lines 4-14, as follows:

The allele specific oligonucleotides (ASO) were designed with the polymorphism approximately in the middle. Oligonucleotides were phosphate free at the 5'end and were purchased from Gibco BRL. Sequences of the oligonucleotides are:

2326 Zmax1.ASO.g: AGACTGGGGTGAGACGC (SEQ ID NO: 63)

D7

2327 Zmax1.ASO.t: CAGACTGGGTTGAGACGCC (SEQ ID NO: 64)

The polymorphic nucleotides are underlined. To label the oligos, 1.5 µl of 1 µg/µl ASO oligo (2326.Zmax1.ASO.g or 2327.Zmax1.ASO.t), 11 µl ddH_2O, 2 µl 10X kinase forward buffer, 5 µl γ-^{32}P-ATP (6000 Ci/mMole), and 1 µl T4 polynucleotide kinase (10 U/µl) were mixed, and the reaction incubated at 37°C for 30-60 minutes. Reactions were then placed at 95°C for 2 minutes and 30 ml H_2O was added. The probes were purified using a G25 microspin column (Pharmacia).

Please replace the paragraph at page 77, line 8 to page 78, line 8, as follows:

The sequence of the human and mouse PCR primers and products were as follows:

Human Zmax1 sense primer (HBM1253) (SEQ ID NO: 65)

CCCGTGTGCTCCGCCGCCCAGTTC

Human Zmax1 antisense primer (HBM1465) (SEQ ID NO: 66)

GGCTCACGGAGCTCATCATGGACTT

Human Zmax1 PCR product (SEQ ID NO: 67)

CCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGC
TGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCTG
CCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTCCTTC
CCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGAC
AGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATG
GGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGGCCC
TTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGT
TCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCC

Mouse Zmax1 Sense primer (HBM1655) (SEQ ID NO: 68)

AGCGAGGCCACCATCCACAGG

Mouse Zmax1 antisense primer (HBM1656) (SEQ ID NO: 69)

TCGCTGGTCGGCATAATCAAT

Mouse Zmax1 PCR product (SEQ ID NO: 70)

AGCAGAGCCACCATCCACAGGATCTCCCTGGAGACTAACAACAACGATGTGGCTATCCCACTC
ACGGGTGTCAAAGAGGCCTCTGCACTGGACTTTGATGTGTCCAACAATCACATCTACTGGACT
GATGTTAGCCTCAAGACGATCAGCCGAGCCTTCATGAATGGGAGCTCAGTGGAGCACGTGATT
GAGTTTGGCCTCGACTACCCTGAAGGAATGGCTGTGGACTGGATGGGCAAGAACCTCTATTGG
GCGGACACAGGGACCAACAGGATTGAGGTGGCCCGGCTGGATGGGCAGTTCCGGCAGGTGCTT
GTGTGGAGAGACCTTGACAACCCCAGGTCTCTGGCTCTGGATCCTACTAAAGGCTACATCTAC
TGGACTGAGTGGGGTGGCAAGCCAAGGATTGTGCGGGCCTTCATGGATGGGACCAATTGTATG
ACACTGGTAGACAAGGTGGGCCGGGCCAACGACCTCACCATTGATTATGCCGACCAGCGA

Please replace the paragraph at page 83, lines 1-11 as follows:

The oligonucleotides designed for Zmax1 are given below:

10875: AGUACAGCUUCUUGCCAACCCAGUC (SEQ ID NO: 71)

10876: UCCUCCAGGUCGAUGGUCAGCCCAU (SEQ ID NO: 72)

10877: GUCUGAGUCCGAGUUCAAAUCCAGG (SEQ ID NO: 73)

Figure 13 shows the results of antisense inhibition of Zmax1 in MC3T3 cells. The three oligonucleotides shown above were transfected into MC3T3 and RNA was isolated according to standard procedures. Northern analysis clearly shows markedly lower steady state levels of the Zmax1 transcript while the control gene GAPDH remained unchanged. Thus, antisense technology using the primers described above allows for the study of the role of Zmax1 expression on bone biology. Similar primers can be used to study Zmax1 expression and its ability to regulate lipid levels in an animal.

IN THE SEQUENCE LISTING

Please replace the Sequence Listing with the Sequence Listing submitted herewith.